

# SEQUENCE LISTING

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## (1) INFORMATION FOR SEQ ID NO:1:

### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

### (ix) FEATURE:

- (B) LOCATION: 2,7
- (D) OTHER INFORMATION: disulfide bridge between  
the Cys residues
- (B) LOCATION: 37
- (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)

(Amidation not shown in sequence)

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Lys	Cys	Asn	Thr	Ala	Thr	Cys	Ala	Thr	Gln	Arg	Leu	Ala	Asn	Phe	Leu
1				5					10					15	
Val	His	Ser	Ser	Asn	Asn	Phe	Gly	Ala	Ile	Leu	Ser	Ser	Thr	Asn	Val
			20					25					30		
Gly	Ser	Asn	Thr	Tyr											
			35												

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acids
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (B) LOCATION: 2,7
- (D) OTHER INFORMATION: disulfide bridge between  
the Cys residues
- (B) LOCATION: 37
- (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)

(Amidation not shown in sequence)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Lys	Cys	Asn	Thr	Ala	Thr	Cys	Ala	Thr	Gln	Arg	Leu	Ala	Asn	Phe	Leu
1				5				10					15		
Ile	Arg	Ser	Ser	Asn	Asn	Leu	Gly	Ala	Ile	Leu	Ser	Pro	Thr	Asn	Val
		20					25					30			
Gly	Ser	Asn	Thr	Tyr											
		35													

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (B) LOCATION: 2,7
- (D) OTHER INFORMATION: disulfide bridge between  
the Cys residues
- (B) LOCATION: 37
- (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)

(Amidation not shown in sequence)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Lys	Cys	Asn	Thr	Ala	Thr	Cys	Ala	Thr	Gln	Arg	Leu	Ala	Asn	Phe	Leu
1				5				10					15		

Val Arg Thr Ser Asn Asn Leu Gly Ala Ile Leu Ser Pro Thr Asn Val  
                     20                    25                    30  
 Gly Ser Asn Thr Tyr  
                     35

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (B) LOCATION: 2,7
- (D) OTHER INFORMATION: disulfide bridge between  
the Cys residues
- (B) LOCATION: 37
- (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)  
(Amidation not shown in sequence)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu  
 1                    5                    10                    15  
 Val Arg Ser Ser Asn Asn Leu Gly Pro Val Leu Pro Pro Thr Asn Val  
                     20                    25                    30  
 Gly Ser Asn Thr Tyr  
                     35

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (B) LOCATION: 2,7
- (D) OTHER INFORMATION: disulfide bridge between  
the Cys residues
- (B) LOCATION: 37

(D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)  
(Amidation not shown in sequence)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Lys	Cys	Asn	Thr	Ala	Thr	Cys	Ala	Thr	Gln	Arg	Leu	Ala	Asn	Phe	Leu
1				5					10					15	
Val	His	Ser	Asn	Asn	Asn	Leu	Gly	Pro	Val	Leu	Ser	Pro	Thr	Asn	Val
			20					25					30		
Gly	Ser	Asn	Thr	Tyr											
			35												

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(B) LOCATION: 2,7

(D) OTHER INFORMATION: disulfide bridge between  
the Cys residues

(B) LOCATION: 37

(D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)

(Amidation not shown in sequence)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Lys	Cys	Asn	Thr	Ala	Thr	Cys	Ala	Thr	Gln	Arg	Leu	Thr	Asn	Phe	Leu
1				5					10					15	
Val	Arg	Ser	Ser	His	Asn	Leu	Gly	Ala	Ala	Leu	Leu	Pro	Thr	Asp	Val
			20					25					30		
Gly	Ser	Asn	Thr	Tyr											
			35												

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(B) LOCATION: 1,6

(D) OTHER INFORMATION: disulfide bridge between  
the Cys residues

(B) LOCATION: 36

(D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)  
(Amidation not shown in sequence)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Cys	Asn	Thr	Ala	Thr	Cys	Ala	Thr	Gln	Arg	Leu	Ala	Asn	Phe	Leu	Val
1			5					10					15		
His	Ser	Ser	Asn	Asn	Phe	Gly	Ala	Ile	Leu	Ser	Ser	Thr	Asn	Val	Gly
			20					25					30		
Ser	Asn	Thr	Tyr												
			35												

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(B) LOCATION: 2,7

(D) OTHER INFORMATION: disulfide bridge between  
the Cys residues

(B) LOCATION: 37

(D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)  
(Amidation not shown in sequence)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Lys	Cys	Asn	Thr	Ala	Thr	Cys	Ala	Thr	Gln	Arg	Leu	Ala	Asn	Phe	Leu
1			5					10					15		
Val	His	Ser	Ser	Asn	Asn	Phe	Gly	Ala	Ile	Leu	Pro	Ser	Thr	Asn	Val
			20					25					30		
Gly	Ser	Asn	Thr	Tyr											
			35												

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(B) LOCATION: 2,7

(D) OTHER INFORMATION: disulfide bridge between  
the Cys residues

(B) LOCATION: 37

(D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)  
(Amidation not shown in sequence)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Lys	Cys	Asn	Thr	Ala	Thr	Cys	Ala	Thr	Gln	Arg	Leu	Ala	Asn	Phe	Leu
1				5					10					15	
Val	His	Ser	Ser	Asn	Asn	Phe	Gly	Pro	Ile	Leu	Pro	Pro	Thr	Asn	Val
			20					25					30		
Gly	Ser	Asn	Thr	Tyr											
			35												

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(B) LOCATION: 2,7

(D) OTHER INFORMATION: disulfide bridge between  
the Cys residues

(B) LOCATION: 37

(D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)  
(Amidation not shown in sequence)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu  
 1 5 10 15  
 Val Arg Ser Ser Asn Asn Phe Gly Pro Ile Leu Pro Ser Thr Asn Val  
 20 25 30  
 Gly Ser Asn Thr Tyr  
 35

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (B) LOCATION: 1,6
  - (D) OTHER INFORMATION: disulfide bridge between  
the Cys residues
  - (B) LOCATION: 36
  - (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
- (Amidation not shown in sequence)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu Val  
 1 5 10 15  
 His Arg Ser Asn Asn Phe Gly Pro Ile Leu Pro Ser Thr Asn Val  
 20 25 30  
 Gly Ser Asn Thr Tyr  
 35

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (B) LOCATION: 2,7
- (D) OTHER INFORMATION: disulfide bridge between  
the Cys residues

(B) LOCATION: 37  
 (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)  
 (Amidation not shown in sequence)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Lys	Cys	Asn	Thr	Ala	Thr	Cys	Ala	Thr	Gln	Arg	Leu	Ala	Asn	Phe	Leu
1				5					10					15	
Val	His	Ser	Ser	Asn	Asn	Phe	Gly	Pro	Val	Leu	Pro	Pro	Thr	Asn	Val
			20					25					30		
Gly	Ser	Asn	Thr	Tyr											
			35												

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (B) LOCATION: 2,7
- (D) OTHER INFORMATION: disulfide bridge between the Cys residues
- (B) LOCATION: 37
- (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)  
 (Amidation not shown in sequence)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Lys	Cys	Asn	Thr	Ala	Thr	Cys	Ala	Thr	Gln	Arg	Leu	Ala	Asn	Phe	Leu
1				5					10					15	
Val	Arg	Ser	Ser	Asn	Asn	Phe	Gly	Pro	Ile	Leu	Pro	Pro	Thr	Asn	Val
			20					25					30		
Gly	Ser	Asn	Thr	Tyr											
			35												

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(B) LOCATION: 1,6

(D) OTHER INFORMATION: disulfide bridge between  
the Cys residues

(B) LOCATION: 36

(D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)

(Amidation not shown in sequence)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Cys	Asn	Thr	Ala	Thr	Cys	Ala	Thr	Gln	Arg	Leu	Ala	Asn	Phe	Leu	Val
1				5				10					15		
Arg	Ser	Ser	Asn	Asn	Phe	Gly	Pro	Ile	Leu	Pro	Pro	Ser	Asn	Val	Gly
			20					25					30		
Ser	Asn	Thr	Tyr												
			35												

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(B) LOCATION: 1,6

(D) OTHER INFORMATION: disulfide bridge between  
the Cys residues

(B) LOCATION: 36

(D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)

(Amidation not shown in sequence)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Cys	Asn	Thr	Ala	Thr	Cys	Ala	Thr	Gln	Arg	Leu	Ala	Asn	Phe	Leu	Val
1				5				10					15		
His	Ser	Ser	Asn	Asn	Phe	Gly	Pro	Ile	Leu	Pro	Pro	Ser	Asn	Val	Gly
			20					25					30		
Ser	Asn	Thr	Tyr												
			35												

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
  - (B) LOCATION: 2,7
  - (D) OTHER INFORMATION: disulfide bridge between  
the Cys residues
  - (B) LOCATION: 37
  - (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
 (Amidation not shown in sequence)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Lys	Cys	Asn	Thr	Ala	Thr	Cys	Ala	Thr	Gln	Arg	Leu	Ala	Asn	Phe	Leu
1				5					10					15	
Val	His	Ser	Ser	Asn	Asn	Leu	Gly	Pro	Val	Leu	Pro	Pro	Thr	Asn	Val
			20					25					30		
Gly	Ser	Asn	Thr	Tyr											
			35												

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
  - (B) LOCATION: 2,7
  - (D) OTHER INFORMATION: disulfide bridge between  
the Cys residues
  - (B) LOCATION: 37
  - (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
 (Amidation not shown in sequence)

Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu  
1 5 10 15  
Val His Ser Ser Asn Asn Leu Gly Pro Val Leu Pro Ser Thr Asn Val  
20 25 30  
Gly Ser Asn Thr Tyr  
35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(Amidation not shown in sequence)

Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu Val  
1 5 10 15  
His Ser Ser Asn Asn Leu Gly Pro Val Leu Pro Ser Thr Asn Val Gly  
20 25 30  
Ser Asn Thr Tyr  
35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(B) LOCATION: 2,7

(D) OTHER INFORMATION: disulfide bridge between  
the Cys residues

(B) LOCATION: 37

(D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)  
(Amidation not shown in sequence)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```
Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu
1          5          10          15
Val Arg Ser Ser Asn Asn Leu Gly Pro Val Leu Pro Ser Thr Asn Val
          20          25          30
Gly Ser Asn Thr Tyr
          35
```

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(B) LOCATION: 2,7

(D) OTHER INFORMATION: disulfide bridge between  
the Cys residues

(B) LOCATION: 37

(D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)  
(Amidation not shown in sequence)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```
Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu
1          5          10          15
Val Arg Ser Ser Asn Asn Leu Gly Pro Ile Leu Pro Pro Thr Asn Val
          20          25          30
Gly Ser Asn Thr Tyr
          35
```

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(B) LOCATION: 2,7

(D) OTHER INFORMATION: disulfide bridge between  
the Cys residues

(B) LOCATION: 37

(D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)

(Amidation not shown in sequence)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Lys	Cys	Asn	Thr	Ala	Thr	Cys	Ala	Thr	Gln	Arg	Leu	Ala	Asn	Phe	Leu
1				5					10					15	
Val	Arg	Ser	Ser	Asn	Asn	Leu	Gly	Pro	Ile	Leu	Pro	Ser	Thr	Asn	Val
			20					25						30	
Gly	Ser	Asn	Thr	Tyr											
				35											

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(B) LOCATION: 2,7

(D) OTHER INFORMATION: disulfide bridge between  
the Cys residues

(B) LOCATION: 37

(D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)

(Amidation not shown in sequence)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Lys	Cys	Asn	Thr	Ala	Thr	Cys	Ala	Thr	Gln	Arg	Leu	Ala	Asn	Phe	Leu
1				5					10					15	
Ile	His	Ser	Ser	Asn	Asn	Leu	Gly	Pro	Ile	Leu	Pro	Pro	Thr	Asn	Val
			20					25						30	
Gly	Ser	Asn	Thr	Tyr											
				35											

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (B) LOCATION: 2,7
- (D) OTHER INFORMATION: disulfide bridge between  
the Cys residues
- (B) LOCATION: 37
- (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)

(Amidation not shown in sequence)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Lys	Cys	Asn	Thr	Ala	Thr	Cys	Ala	Thr	Gln	Arg	Leu	Ala	Asn	Phe	Leu
1				5				10					15		
Val	Ile	Ser	Ser	Asn	Asn	Phe	Gly	Pro	Ile	Leu	Pro	Pro	Thr	Asn	Val
			20				25						30		
Gly	Ser	Asn	Thr	Tyr											
			35												

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (B) LOCATION: 1,6
- (D) OTHER INFORMATION: disulfide bridge between  
the Cys residues
- (B) LOCATION: 36
- (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)

(Amidation not shown in sequence)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu Ile



(D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)  
(Amidation not shown in sequence)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Lys	Cys	Asn	Thr	Ala	Thr	Cys	Ala	Thr	Gln	Arg	Leu	Ala	Asn	Phe	Leu
1				5					10					15	
Ile	Arg	Ser	Ser	Asn	Asn	Leu	Gly	Ala	Val	Leu	Ser	Pro	Thr	Asn	Val
			20				25						30		
Gly	Ser	Asn	Thr	Tyr											
			35												

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (B) LOCATION: 2,7
- (D) OTHER INFORMATION: disulfide bridge between  
the Cys residues
- (B) LOCATION: 37
- (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)  
(Amidation not shown in sequence)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Lys	Cys	Asn	Thr	Ala	Thr	Cys	Ala	Thr	Gln	Arg	Leu	Ala	Asn	Phe	Leu
1				5					10					15	
Ile	Arg	Ser	Ser	Asn	Asn	Leu	Gly	Pro	Val	Leu	Pro	Pro	Thr	Asn	Val
			20				25						30		
Gly	Ser	Asn	Thr	Tyr											
			35												

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein



(ix) FEATURE:  
 (B) LOCATION: 2,7  
 (D) OTHER INFORMATION: disulfide bridge between  
 the Cys residues  
 (B) LOCATION: 37  
 (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)  
 (Amidation not shown in sequence)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Lys	Cys	Asn	Thr	Ala	Thr	Cys	Ala	Thr	Gln	Arg	Leu	Thr	Asn	Phe	Leu
1				5				10						15	
Val	His	Ser	Ser	His	Asn	Leu	Gly	Ala	Ala	Leu	Leu	Pro	Thr	Asp	Val
		20					25						30		
Gly	Ser	Asn	Thr	Tyr											
		35													

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:  
 (B) LOCATION: 2,7  
 (D) OTHER INFORMATION: disulfide bridge between  
 the Cys residues  
 (B) LOCATION: 37  
 (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)  
 (Amidation not shown in sequence)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Lys	Cys	Asn	Thr	Ala	Thr	Cys	Ala	Thr	Gln	Arg	Leu	Thr	Asn	Phe	Leu
1				5				10						15	
Val	His	Ser	Ser	His	Asn	Leu	Gly	Ala	Ala	Leu	Ser	Pro	Thr	Asp	Val
		20					25						30		
Gly	Ser	Asn	Thr	Tyr											
		35													

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(B) LOCATION: 1,6

(D) OTHER INFORMATION: disulfide bridge between  
the Cys residues

(B) LOCATION: 36

(D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)

(Amidation not shown in sequence)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Cys	Asn	Thr	Ala	Thr	Cys	Ala	Thr	Gln	Arg	Leu	Thr	Asn	Phe	Leu	Val
1				5				10					15		
His	Ser	Ser	His	Asn	Leu	Gly	Ala	Val	Leu	Pro	Ser	Thr	Asp	Val	Gly
			20					25					30		
Ser	Asn	Thr	Tyr												
			35												

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(B) LOCATION: 2,7

(D) OTHER INFORMATION: disulfide bridge between  
the Cys residues

(B) LOCATION: 37

(D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)

(Amidation not shown in sequence)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Lys	Cys	Asn	Thr	Ala	Thr	Cys	Ala	Thr	Gln	Arg	Leu	Thr	Asn	Phe	Leu
1				5				10					15		
Val	Arg	Ser	Ser	His	Asn	Leu	Gly	Ala	Ala	Leu	Ser	Pro	Thr	Asp	Val
			20					25					30		
Gly	Ser	Asn	Thr	Tyr											
			35												

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (B) LOCATION: 2,7
- (D) OTHER INFORMATION: disulfide bridge between  
the Cys residues
- (B) LOCATION: 37
- (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)  
(Amidation not shown in sequence)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Lys	Cys	Asn	Thr	Ala	Thr	Cys	Ala	Thr	Gln	Arg	Leu	Thr	Asn	Phe	Leu
1				5				10						15	
Val	Arg	Ser	Ser	His	Asn	Leu	Gly	Ala	Ile	Leu	Pro	Pro	Thr	Asp	Val
			20				25						30		
Gly	Ser	Asn	Thr	Tyr											
		35													

(2) INFORMATION FOR SEQ ID NO:33

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (B) LOCATION: 2,7
- (D) OTHER INFORMATION: disulfide bridge between  
the Cys residues
- (B) LOCATION: 37
- (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)  
(Amidation not shown in sequence)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Thr Asn Phe Leu  
 1 5 10 15  
 Val Arg Ser Ser His Asn Leu Gly Pro Ala Leu Pro Pro Thr Asp Val  
 20 25 30  
 Gly Ser Asn Thr Tyr  
 35

(2) INFORMATION FOR SEQ ID NO:34

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (B) LOCATION: 2,7
- (D) OTHER INFORMATION: cyclo linkage between the Asp  
and Lys residues
- (B) LOCATION: 37
- (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)

(Amidation not shown in sequence)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Lys Asp Asn Thr Ala Thr Lys Ala Thr Gln Arg Leu Ala Asn Phe Leu  
 1 5 10 15  
 Val His Ser Ser Asn Asn Phe Gly Ala Ile Leu Ser Ser Thr Asn Val  
 20 25 30  
 Gly Ser Asn Thr Tyr  
 35

(2) INFORMATION FOR SEQ ID NO:35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (B) LOCATION: 2,7
- (D) OTHER INFORMATION: disulfide bridge between

the Cys residues

(B) LOCATION: 37

(D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)  
(Amidation not shown in sequence)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Ala	Cys	Asn	Thr	Ala	Thr	Cys	Ala	Thr	Gln	Arg	Leu	Ala	Asn	Phe	Leu
1				5					10					15	
Val	His	Ser	Ser	Asn	Asn	Phe	Gly	Ala	Ile	Leu	Ser	Ser	Thr	Asn	Val
			20					25					30		
Gly	Ser	Asn	Thr	Tyr											
			35												

(2) INFORMATION FOR SEQ ID NO:36

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(B) LOCATION: 2,7

(D) OTHER INFORMATION: disulfide bridge between  
the Cys residues

(B) LOCATION: 37

(D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)  
(Amidation not shown in sequence)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Ser	Cys	Asn	Thr	Ala	Thr	Cys	Ala	Thr	Gln	Arg	Leu	Ala	Asn	Phe	Leu
1				5					10					15	
Val	His	Ser	Ser	Asn	Asn	Phe	Gly	Ala	Ile	Leu	Ser	Ser	Thr	Asn	Val
			20					25					30		
Gly	Ser	Asn	Thr	Tyr											
			35												

(2) INFORMATION FOR SEQ ID NO:37

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(B) LOCATION: 2,7

(D) OTHER INFORMATION: disulfide bridge between  
the Cys residues

(B) LOCATION: 37

(D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)

(Amidation not shown in sequence)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

[illegible]

(2) INFORMATION FOR SEQ ID NO:38

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(B) LOCATION: 2,7

(D) OTHER INFORMATION: disulfide bridge between  
the Cys residues

(B) LOCATION: 37

(D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)

(Amidation not shown in sequence)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

[illegible]

## (2) INFORMATION FOR SEQ ID NO:39

Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu Val  
1 5 10 15  
His Ser Ser Asn Asn Phe Gly Pro Ile Leu Pro Ser Thr Asn Val Gly  
20 25 30  
Ser Asn Thr Tyr  
35

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 36 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:  
 (B) LOCATION: 1,6  
 (D) OTHER INFORMATION: disulfide bridge between  
 the Cys residues  
 (B) LOCATION: 36  
 (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)  
 (Amidation not shown in sequence)

65

Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu Val  
1 5 10 15  
His Ser Ser Asn Asn Phe Gly Pro Val Leu Pro Pro Ser Asn Val Gly  
20 25 30  
Ser Asn Thr Tyr  
35

(2) INFORMATION FOR SEQ ID NO:41

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (B) LOCATION: 2,7
  - (D) OTHER INFORMATION: disulfide bridge between the Cys residues
  - (B) LOCATION: 11
  - (D) OTHER INFORMATION: Arg is a D amino acid residue
  - (B) LOCATION: 37
  - (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
- (Amidation not shown in sequence)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu  
1 5 10 15  
Val His Ser Ser Asn Asn Phe Gly Ala Ile Leu Ser Ser Thr Asn Val  
20 25 30  
Gly Ser Asn Thr Tyr  
35